

1 GGTATTTCAG GCCATGGTGT TCGCGCCGAAT TAATTCCCGA TCCAGACATG ATAAGATACA TTGATGAGTT TGGACAAACC ACAACTAGAA TGCAGTGAAA  
CAATAAAGTC CGGTACCACA ACGCGGCTTA ATTAAGGCT AGGTCTGTAC TATTCTATGT AACTACTCAA ACCTGTTGG TGTGATCTT ACGTCACTTT  
(SEQ ID NO: 1)

101 AAAATGCTTT ATTGTGAAA TTTGTGATGC TATTGCTTTA TTTGTAACCA TTATAAGCTG CAATAAACAA GTTGGCCAT GCGGGCCAAG CTTCGACAG  
TTTTACGAAA TAAACACTTT AAACACTACG ATAACGAAAT AAACATTGGT AATATTCGAC GTTATTGTT CAACCCGGTA CCGCCGGTTC GAAGACGTCC

201 TCGACTCTAG AGGATCCCCG GGAATTCCG GCATGACTCG ATCGCCGCC CTAAGAGAGC TGCCCCCGAG TTACACACC CCAGCTCGAA CCGCAGCACC  
AGCTGAGATC TCCTAGGGC CCCTTAAGC CGTACTGAGC TAGCGGGG GAGTCTCTCG ACGGGGCTC AATGTGTGG GGTGAGCTT GCGTCTGTG  
M T R S P P L R E L P P S Y T P P A R T A A P  
(SEQ ID NO: 2)

301 CCAGATCCTA GCTGGGAGCC TGAAGGCTCC ACTCTGGCTT CGTGCTTACT TCCAGGGCTT GCTCTCTCT CTGGGATGCG GGATCCAGAG ACATTGTGGC  
GGTCTAGGAT CGACCTCGG ACTTCCGAGG TGAGACCGAA GCACGAATGA AGGTCCCGGA CGAGAAGAGA GACCTACGC CTAAGTCTC TGTAAACACC CATCTTACC

401 AAAAGTCTCT TTCTGGACT GTTGGCTTT GGGGCCCTGG CATTAGGTCT CCGATGGCC ATTATTGAGA CAAACTTGA ACAGCTCTCG GTAGAAGTGG  
TTTACGAGA AAGACCTGA CAACCGGAAA CCGCGGACC GTAATCCAGA GCGTACCGG TAATAACTCT GTTGAACCT TGTGAGAGC CATCTTACC

57 K V L F L G L L A F L A F G A L A L G L R M A I I E T N L E Q L W V E V G  
501 GAGCCGGT GAGCCAGGAG CTGCATTACA CCAAGGAGAA GCTGGGGAG GAGGTGCTAT ACACCTCTCA GATGCTGATA CAGACCGCAC GCCAGAGGG  
CGTCGGCCCA CTCGCTCTC GACGTAATGT GTTCTCTCTT CGACCCCTC CTCCGACGTA TGTGAGAGT CTACGACTAT GTCTGGCGTG CCGTCTCTCC

91 S R V S Q E L H Y T K E K L G E A A Y T S Q M L I Q T A R Q E G  
601 AGAGAACATC CTCACACCCG AAGCACTTG AAGCACTTG CCTCCACCTC CAGGCAGCC TCACTGCCAG TAAAGTCCAA GTATCACTCT ATGGGAAGTC CTGGGATTG  
TCTCTGTAG GAGTGTGGC TTCTGTAACC GGAGGTGGAG GTCCGTGGG AGTGACGTC ATTTCAGGTT CATAGTGAGA TACCCTTCAG GACCTAAAC

124 E N I L T P E A L G L H L Q A A L T A S K V Q V S L Y G K S W D L  
701 AACAAAATCT GCTACAAGTC AGGAGTTCCC CTATTGAAA ATGGAATGAT TGAGTGGATG ATTGAGAAGC TGTTCCTG CGTATCCTC ACCCCCTCG  
TTGTTTGA CGATGTTTCA TCCTCAAGG GAATAACTTT TACCTTACTA ACTCACCTAC TAACCTCTCG ACAAGGCAC GCACTAGGAG TGGGGGAGC

157 N K I C Y K S G V P L I E N G M I E W M I E K L F P C V I L T P L D  
801 ACTGCTTCTG GAGGGAGCC AAACCTCCAG GGGCTCCG CTACCTGCC GCGCGCCCG ATATCCAGT GACCAACCTG GATCCAGAGC AGCTGCTGA  
TGACGAAGAC CTTCTCTCG TTTGAGGTC CCGGAGGCG GATGACGGG CCGCGGCGG TATAGTCACT CTGTTGGAC CTAGGTCTG TCGACGACCT

191 C F W E G A K L Q G G S A Y L P G R P D I Q W T N L D P E Q L L E

FIG. 1A

901 GGAGCTGGGT CCCTTTGCT CCCTTGAGGG CTGCTAGACA AGGCACAGGT GGGCCAGGCC TACGTGGGC GGCCTGTCT GCACCTGTAT  
 CCTCGACCCA GGGAAACGGA GGGAACTCCC GAAGGCCCTC GACGATCTGT TCCGTGTCCA CCGGTCCGG ATGCACCCCG CCGGACAGA CGTGGGACTA  
 224 E L G P F A S L E G F R E L L D K A Q V G Q A Y V G R P C L H P D  
 224 GACCTCCACT GCGGCTGATC ACGGGGTTG GTAGTGTCT GGTCCGAGG GTTACACCGA GTGCTCGACT CACCCCGAC GGTACCGAAG AGGTGTTTA  
 1001 GACCTCCACT GCGGCTGATC ACGGGGTTG GTAGTGTCT GGTCCGAGG GTTACACCGA GTGCTCGACT CACCCCGAC GGTACCGAAG AGGTGTTTA  
 CTGAGAGTGA CCGGTGGATC ACGGGGTTG GTAGTGTCT GGTCCGAGG GTTACACCGA GTGCTCGACT CACCCCGAC GGTACCGAAG AGGTGTTTA  
 257 D L H C P P S A P N H H S R Q A P N V A H E L S G G C H G F S H K F  
 257 TCAATGCTG CAGAGCTGA GTGGGGGCTG CACAGCTGA GTGGGGGCTG CACAGCTGA GTGGGGGCTG CACAGCTGA GTGGGGGCTG CACAGCTGA  
 1101 TCAATGCTG CAGAGCTGA GTGGGGGCTG CACAGCTGA GTGGGGGCTG CACAGCTGA GTGGGGGCTG CACAGCTGA GTGGGGGCTG CACAGCTGA  
 AGTACGTGAC CGTCTCTCTT AACGACGACC CTCCGTACCG GTCTCTCTCG GTTCTCTCTCG GTTCTCTCTCG GTTCTCTCTCG GTTCTCTCTCG  
 291 M H W Q E E L L L G G M A R D P Q G E L L R A E A L Q S T F L L M  
 1201 GAGTCCCCGC CAGCTGTACG AGCATTTCCG GGGTACTAT CAGACACATG ACATTGGCTG GAGTGAGGAG CAGGCACGCA CAGTGCTACA AGCCTGGCAG  
 CTCAGGGGCG GTCGACATGC TCGTAAAGGC CCGACTGATA GTCTGTGTAC GTTAACCGAC CTCACTCTCTC GTCCGGTCTG GTCACGATGT TCGGACCGTC  
 324 S P R Q L Y E H F R G D Y Q T H D I G W S E E Q A S T V L Q A W Q  
 1301 CGGCGCTTG TGCAGTGGC CCAGGAGGCC CTGCTCTAGA ACGTTTCCA GCAGATCCAT GCCTTCTCTCT CCACACCCCT GGATGACATC CTGCTGCTGCT  
 GCGCGGAAAC ACGTCGACCG GGTCTCTCCG GACGGACTCT TCGAAGGGT CGTCTAGTA CGGAAGAGGA GGTGGTGGGA CCTACTGTAG GACGTACGCA  
 357 R F V Q L A Q E A L P E N A S Q Q I H A F S S T T L D I L H A F  
 1401 TCTCTGAAGT CAGTGTGCTGCG CGTGTGGTGG GAGGCTATCT GCTCATGCTG GCCTATGCTG GTGTGACAT CTTGCGGCTG GACTGCGGCC AGTCCCAGGG  
 AGAGACTTCA GTCACGACCG GCACACCCACC CTCCGATAGA CGAGTACGAC CGGATACGGA CACACTGGTA CGACGCCACC CTGACCGCGG TCAGGGTCCC  
 391 S E V S A A R V V G G Y L L M L A Y A C V T M L R W D C A Q S Q G  
 1501 TTCCGTGGC CTGCGCGGG TACTGTGCTG TACTGTGCTG TACTGTGCTG TACTGTGCTG TACTGTGCTG TACTGTGCTG TACTGTGCTG TACTGTGCTG  
 AAGGCACCG GAACGGCCCC ATGACGACCA CCGGACCGC CACCGGAGTC CGGAACCCGA GCAGCGGAC GACCGGTAGT GGAAGTTACG ACGGTGATGG  
 424 S V G L A G V L L V L L V A L A V A S G L G L C A L L G I T F N A A T T  
 1601 CAGGTGCTGC CTCTCTTGGC TCTGGGAATC GCGTGGATG ACCTATTCCT GCTGGGCTG GCCTTCACAG AGGCTCTGCC TGGCACCCCT CTCAGGAGC  
 GTCCACGACG GAAGAACCG AGACCCCTTAG CCGACCTAC TGCATAAGGA CGACCGCGTA CGGAAGTGT TCCGAGACCG ACCGTGGGA GAGTCTCTCG  
 457 Q V L P F L A L G I G V D D V F L L A H A F T E A L P G T P L Q E R  
 1701 GCATGGGCGA GTGTCTGAG CGCAGGGGCA CCACTGTCTG ACTCACATCC ATCAACAACA TGGCCGCTCT CCTCATGGCT GCCCTCGTTC CCATCCCTGC  
 CGTACCCGCT CACAGACGTC GCGTGGCCGT GTGTCTGAG GTGTCTGAG GTGTCTGAG GTGTCTGAG GTGTCTGAG GTGTCTGAG GTGTCTGAG GTGTCTGAG  
 491 M G E C L Q R T G T S I N N M A A F L M A A L V P I P A

FIG. 1B

1801 GCTGGAGCC TTCTCCCTAC AGGCGGCCAT AGTGGTTGGC TGCACCTTTG TAGCCGTGAT GCTTGTCTTC CCAGCCATCC TCAGCCTGGA CCTACGGCGG  
CGACGCTCGG AAGAGGGATG TCCGCCGGTA TCACCAACCG ACGTGGAAAC ATCGGCACCTA CGAACAGAAG L V F P A I L S L D L R R

524 L R A F S L Q A A I V V G C T F V A V M L V F P A I L S L D L R R

1901 CGCCACTGCC AGCGCCTTGA TGTGCTCTGC TGCTCTCTCA GTCCCTGCTC TGCTCAGGTG ATTCAGATCC TGCCCCAGGA GCTGGGGGAC GGGACAGTAC  
GCGGTGACGG TCGCGGAAT ACACGAGACG ACGAAGAGGT CAGGACGAG ACAGTCCAC TAAGTCTAGG ACGGGTCTC CGACCCCTG CCCTGTCTATG

557 R H C Q R L D V L C C F S S P C S A Q V I Q I L P Q E L G D G T V P

2001 CAGTGGGCAT TGCCACCTC ACTGCCACAG TTCAAGCCTT TACCCACTGT GAAGCCAGCA GCCAGCATGT GGTACCATC CTGCTCTCCC AAGCCCACT  
GTCACCCGTA ACGGTGGAG TGACGGTGT AAGTTCGGAA ATGGGTGACA CTTCCGGTCTG CCGTCTGACA CCAGTGGTAG GACGGAGGGG TTCGGGTGGA

591 V G I A H L T A T V Q A F T H C E A S S Q H V V T I L P P Q A H L

2101 GGTGCCCCCA CCTTCTGACC CACTGGGCTC TGAGCTCTTC AGCCTGGAG GGTCCACACG GGACCTTCTA GGCAGGAGG AGGAGACAAG GCAGAAGGCA  
CCACGGGGGT GGAAGACTGG GTGACCCGAG ACTCGAGAAG TCGGACCTC CCAGGTGTGC CCTGGAAGAT CCGTCTCTC TCCTCTGTT CCGTCTCTCGT

624 V P P P S D P L G S E L F S P G G S T R D L L G Q E E T R Q K A

2201 GCCTGGAAGT CCCTGCCCTG TGCCCGCTGG AATCTTGCCC ATTTGCCCC CTATCAGTT GCCCGGTGC TGCTCAGTC ACATGCCAAG GCATCTGTGC  
CGACGTTCA GGGACGGGAC ACGGGGACC TTAGAACGGG TAAAGCGGC GATAGTCAA CCGGGCAACG ACGAGGTGAG TGACGGTTC CCGTAGCAGG

657 A C K S L P C A R W N L A H F A R Y Q F A P L L L Q S H A K A I V L

2301 TGGTGCTCTT TGGTGCTCTT CTGGGCTTGA GCCTCTACGG AGCCACCTTG GTGCAAGACG GCCTGGCCCT GACGGATGTG GTGCTCTGGG GCACCAAGGA  
ACCACGAGAA ACCACGAGAA GACCTGGGG TCGAGTCCAT GAAGAGGGAC ATGCTCCACC GGGACCACTG GGTCCCAACG AAAGTGTG CCGGAGGCC CCGTGTCTC

691 V L F G A L L G L S L Y G A T L V Q D G L A L T D V V P R G T K E

2401 GCATGCCCTC CTGAGCGCCC AGCTCAGGTA CTCTCTCCCTG TACGAGGTGG CCCTGGGTGAC CCAGGTGGC TTTGACTACG CCCATTCCA ACGGCCCTC  
CGTACGGAAG GACTCGGGG TCGAGTCCAT TCGAGTCCAT GAAGAGGGAC ATGCTCCACC GGGACCACTG GGTCCCAACG AAAGTGTG CCGGAGGCC CCGTGTCTC

724 H A F L S A Q L R Y F S L Y E V A L V T Q G G F D Y A H S Q R A L

2501 TTTGATCTGC ACCAGCGCTT CAGTTCCCTC AAGGCGGTGC TGCCCCCACC GGCCACCCAG GCACCCCGCA CCTGGCTGCA CTATTACCGC AACTGGCTAC  
AAACTAGACG TGGTCCGAA GTCAAGGGAG TTCCGCCACG ACGGGGTGG CCGGTGGTC CCGTGGCGGT GGACCGACGT GATAATGGCG TTGACCGATG

757 F D L H Q R F S S L K A V L P P A T Q A P R T W L H Y Y R N W L Q

2601 AGGGAATCCA GGCTGCTCTT GACCAAGACT GGGCTTCTGG GCGCATCACC CGCCACTCGT ACCGCAATGG CTCTGAGGAT GGGGCCCTGG CCTACAAGCT  
TCCCTTAGGT CCGACGGAA CTGGTCTCTGA CCGAAGACC CCGGTAGTG GCGGTGAGCA TGGCGTTACC GAGACTCTCA CCGCGGAC GATGTCTGA

791 G I Q A A F D Q D W A S G R I T R H S Y R N G S E D G A L A Y K L

FIG. 1C

2701 GCTCATCCAG ACTGGAGACG CCCAGGAGCC TCTGGATTTC AGCCAGCTGA CCACAAGGAA GCTGGTGGAC AGAGAGGGAC TGATCCACC CGAGCTCTTC  
 CGAGTAGGTC TGACCTCTGC GGGTCTCGG AGACCTAAG TCGGTGCACT GGTGTTCTT CGACCACCTG TCTCTCCCTG ACTAAGTGG GCTCGAGAAG  
 824 L I Q T G D A Q E P L D F S Q L T T R K L V D R E G L I P P E L F  
 2801 TACATGGGGC TGACCGTGTG GGTGAGCAGT GACCCCTGG GTCTGGCAGC CTCACAGCC AACTTCTACC CCCACCTCC TGAATGGCTG CACGACAAAT  
 ATGTACCCCG ACTGGCACAC CCACTCGTCA CTGGGGGACC CAGACCGTCG GAGTGTCCGG TTGAAGATGG GGGTGGAGG ACTTACCGAC GTGCTGTTTA  
 857 Y M G L T V W V S S D P L G L A A S Q A N F Y P P P P E W L H D K Y  
 2901 ACGACACCAC GGGGGAGAAC CTTCCGATCC CGCCAGCTCA GCGCTTGGAG TTGCCCCAGT TCCCTTCTCT GCTGCGTGGC CTCAGAAGA CTGCAGACTT  
 TGCTGTGGTG CCCCCCTTGG GAAGCGTAGG GCGGTGAGT CCGGAACCTC AAACGGGTCA AGGGGAAGGA CGACGCACCG GAGTCTTCT GACGTCTGAA  
 891 D T T G E N L R I P P A Q P L E F A Q F P F L L R G L Q K T A D F  
 3001 TGTGAGGCC ATCGAGGGG CCCGGCAGC ATGCGGAGAG GCGGGCCAG CTGGGTGCA CGCCTACCCC AGCGTCCC CTTCTCTCTT CTGGGAACAG  
 ACACCTCCGG TAGCTCCCC GGGCCGTCG TACGCGTCTC CGGCCGCTC A G Q A G V H A Y P S G S P F L F W E Q  
 924 V E A I E G A R A A C A E A G Q A G V H A Y P S G S P F L F W E Q  
 3101 TATCTGGGCC TGGGGCGCTG CTTCTCTGTA GCGGTCTGCA TCCTGCTGGT GTGCACCTTC CTGCTCTGTG CTCTGCTGCT CTTCAACCCC TGGACGGCTG  
 ATAGACCCCG ACCCGCGAC GAAGACGAC CCGCAGACGT AGGACGACCA CACGTGAAG GAGCAGACAC GAGACGACGA GGAGTGGGG ACCTGCCGAC  
 957 Y L G L R R C F L L A V C I L L V C T F L V C A L L L L N P W T A G  
 3201 GCCTCATAGT GCTGGTCTG GCGATGATGA CAGTGAACCT CTTTGGTATC ATGGGTCTCC TGGGCATCAA GCTGAGTGCC ATCCCCGCTG TGATCCTTGT  
 CCGAGTATCA CGACAGGAC CGCTACTACT GTCACCTTGA GAAACCATAG TACCCAAAGG ACCCGTAGTT CGACTCAGG TAGGGGCACC ACTAGGAACA  
 991 L I V L V L A M T V E L F G I M G F L G I K L S A I P V V I L V  
 3301 GGCCTCTGTA GGCATTGGG TTGAGTTCAC AGTCCACGTG GCTCTGGGCT TCCTGACCAC CCAGGCAGC CGAACCTGC GGGCCGCCCA TGCCCTTGAG  
 CCGGAGACAT CCGTAACCGC AACTCAAGT TCAAGTGCAC CGAGACCCGA AGGACTGGTG GGTCCCGTCG GCCTTGACG CCCGGCGGT ACGGAACTC  
 1024 A S V G I G V E F T V H V A L G F L T T Q G S R N L R A A H A L E  
 3401 CACACATTTG CCCCCTGAC CGATGGGGCC ATCTCCACAT TGCTGGGTCT GCTCATGCTT GCTGGTCCC ACTTTGACTT CATGTGAAGG TACTTCTTTG  
 GTGTGTAAC GGGGGCACTG GCTACCCCGG TAGAGTGTA ACGACCCAGA CGAGTACGAA CGACCAAGG TGAAACTGAA GTAACATTCC ATGAAGAAC  
 1057 H T F A P V T D G A I S T L L G L L M L A G S H F D F I V R Y F F A  
 3501 CGCGGCTGAC AGTGTCTACG CTCTCGATGG TCCTCCATGG ACTCGTGTG CTGCCTGTG TGCTGTCCAT CCTGGGCCCG CCGCCAGAGG TGATACAGAT  
 GCGCGGACTG TCACGAGTGC GAGGACCCCG AGGAGGTACC TGAGCACGAC GACGACACG ACACAGGTA GGACCCCGGC GCGGTCTCC ACTATGTCTA  
 1091 A L T V L T L L G L L H G L V L L P V L L S I L G P P P E V I Q M

FIG. 1D

```

3601 GTACAAGGAA AGCCACAGAGA TCCTGAGTCC ACCAGCTCCA CAGGAGGCG GGCTTAGGTG GGGGGCATCC TCCTCCCTGC CCCAGAGCTT TGCAGAGTG
CATGTTCCCTT TCGGGTCTCT AGGACTCAGG TGGTCGAGGT GTCCCTCCGC CCGAATCCAC CCCCCTAGG AGGAGGGACG GGTCTCGAA ACGTCTCAC
1124 Y K E S P E I L S P P A P Q G G G L R W G A S S L P Q S F A R V
1124 Y K E S P E I L S P P A P Q G G G L R W G A S S L P Q S F A R V
3701 ACTACCTCCA TGACCGTGGC CATCCACCCA CCCCCTCTGC CTGGTGCCTA CATCCATCCA GCCCTGATG AGCCCCCTTG GTCCCTGCT GCCACTAGCT
TGATGGAGGT ACTGGCACCG GTAGGTGGGT GGGGGGACG GACCACGGAT GTAGGTAGGT A P D E P P W S P A A T S S
1157 T T S M T V A I H P P P L P G A Y I H P A P D E P P W S P A A T S S
3801 CTGGCAACCT CAGTTCAGG GGACCAAGTC CAGCCACTGG GTGAAAGAGC AGCTGAAGCA CAGAGACCAT GTGTGGGCG TGTGGGTCA CTGGGAAGCA
GACCGTTGGA GTCAAGGTCC CCTGGTCCAG GTCGGTGACC CACTTCTCG TCGACTTCGT GTCTCTGGTA CACACCCCGC ACACCCAGT GACCCCTTCGT
1191 G N L S S R G P G P A T G O 1203
3901 CTGGGTCTGG TGTTAGACGC AGGACGGACC CCTGGAGGC CCTGCTGCTG CTGCATCCC TCTCCGACC CAGCTGTCT GGGCTCCCT GATATCGAAT
GACCCAGACC ACAATCTGCG TCCTGCCTGG GGACCTCCCG GGACGACGAC GACGTAGGG AGAGGCTGG GTCGACAGTA CCGGAGGGA CTATAGCTTA
^T to C (silent) pRK follows, this is the 5prime end of vector^
4001 TCAATCGATA GAACCGAGGT GCAGTTGGAC
AGTTAGCTAT CTTGGCTCCA CGTCAACCTG

```

FIG. 1E

(SEQ ID NO: 3)

	30	40	50	60	70
905531	GCTGGGGTGCACGCCTACCNACAGCGGNTCCCCCTTCCTCTTCTGGGAACA				
	:::	::	:	*****	*****
hpatched	CTGGGGCTGTCCAGTTACCCCAACGGCTACCCCTTCCTCTTCTGGGAGCA				

(SEQ ID NO: 4)

	3010	3020	3030	3040	3050
905531	GTATCTGGGCCTGCGGCGCTGCTTCCTGCTGGCCGCTCTGCATCCTGCTGG				
	***	*	*****	*	*****
hpatched	GTACATCGGCCTCCGCCACTGGCTGCTGCTGTTTCATCAGCGTGGTGTGG				

	3060	3070	3080	3090	3100
905531	TGTGCACTTTCCTCGTCTGTGCTCTGCTGCTCCTNAACCCCTGGACGGCT				
	*****	*****	*****	*****	*****
hpatched	CCTGCACATTTCCTCGTGTGCGCTGTCTTCCTTCTGAACCCCTGGACGGCC				

	3110	3120	3130	3140	3150
905531	GGCCTNATAGTGCTGGTTCCTGGCGATGATGACAGTGGAACTCTTTGGTAT				
	**	*****	*****	*****	*****
hpatched	GGGATCATTGTGATGGTTCCTGGCGCTGATGACGGTCGAGCTGTTTCGGCAT				

	3160	3170	3180	3190	3200
905531	CATGGGTTTNCCTGGGCATCAAGCTGAGT				
	*****	*****	*****	*****	*****
hpatched	GATGGGCCTCATCGGAATCAAGCTCAGT				

	3210	3220	3230		
--	------	------	------	--	--

	80	90	100	110	120
905531	TCTGGGCCTGCGGCGCTGCTTCCTGCTGGCCGCTCTGCATCCTGCTGGTGT				
	:::	:::	* * *	* * *	*****
hpatched	GCTGCTGCTGTTTCATCAGCGTGGTGTGGCC--TGCACATTTCCTCGTGT				

	3090	3100	3110	3120
--	------	------	------	------

	130	140	150
905531	GCACTTTCCTCGTCTGTGCTCTGCTGCT		
	**	*	*
hpatched	GCGCTGTCTTCCTTCTGAACCCCTGGAC		

	3130	3140	3150
--	------	------	------

FIG. 2A

(SEQ ID NO: 5) 1326258 30 40 50 60 70  
 GCTGGGGTGCACGCCCTACCCAGCGGCTCCCCCTTCCTCTCTGGAACA  
 :::: : \*\*\*\*\*  
 hpatched CTGGGGCTGTCCAGTTACCCCAACGGCTACCCCTTCCTCTCTGGAACA  
 3010 3020 3030 3040 3050

1326258 80 90 100 110 120  
 GTATCTGGGCCTGCGGCGCTGCTTCCTGCTGGCCGTCTGCATCCTGCTGG  
 \*\*\* \* \*\*\*\*\* \* \* \* \* \*  
 hpatched GTACATCGGCCTCCGCCACTGGCTGCTGCTGTTTCATCAGCGTGGTGTGG  
 3060 3070 3080 3090 3100

1326258 130 140 150  
 TGTGCACTTTCCTCNTCTGTGCTCT  
 \*\*\*\*\*  
 hpatched CCTGCACATTCCTCGTGTGCGCTGT  
 3110 3120 3130

1326258 90 100 110 120 130  
 TCTGGGCCTGCGGCGCTGCTTCCTGCTGGCCGTCTGCATCCTGCTGGTGT  
 :::: : \* \* \* \* \*  
 hpatched GCTGCTGCTGTTTCATCAGCGTGGTGTGGCC---TGCACATTCCTCGTGT  
 3090 3100 3110 3120

1326258 140 150  
 GCACTTTCCTCNTCTGTGCTCT  
 \*\* \* \* \* \* :  
 hpatched GCGCTGTCTTCCTTCTGAACCC  
 3130 3140

1326258 10 20 30 40 50  
 CCGGGCAGCATGCGCAGAGGCCGGCCAGGCTGGGGTGCACGCCCTACCCCA  
 \*\*\*\*\* \* \* \* \* \*  
 (SEQ ID NO 6) hpatched.RC CCGGGCGGCATG--GCGAAGCGGACCACGCTGGGGGGTGGCTCAGGGGAG  
 710 720 730 740 750

FIG. 2B

(SEQ ID NO:4) PTCH 1 MASAGNAEPQDRGGGGGCGICAGPRAGGRRRTGGLRRAA[PDR]DYL  
(SEQ ID NO:2) PTCH2 1 . . . . .

PTCH 51 HRPSYCDAAF[AL]EQISKGA[AT]GRKAPLWLR[KFQ]RLL[FK]LGC[YIQ]KN[CGK]  
PTCH2 11 -PSYTPP..[ART]AAPQIL[A]GSL[KAPLWLR[YFQ]GLL[FS]LGC[G]LQRH[CGK]

TM1

PTCH 101 FLVVGLLIFGA[FAV]GLKA[ANL]ETN[V]EELWVEVG[GRVSR]ELNYT[RQK]IGEE  
PTCH2 58 VLFLGLLAFGALLALGLRMA[II]ETNLEQLWVEVGS[RV]SQELHYT[KEK]LGEE

PTCH 151 AMFNPLQIMIQTPKEEGANVLTTEALQHLDSALQASRVHVMYNRQWKL[E]  
PTCH2 108 AAYTSQMLIQIQTARQEGENILTP[EA]LGLHLQAL[TASKV]QVSLY[GK]SWDLN

PTCH 201 HLCYKSGELITETGYMDQIIEYLYPCLIIITPLDCFWEGAKLQSGTAYLLG  
PTCH2 158 KLCYKSGVPLIENGMI[EW]IEKLFPCVILITPLDCFWEGAKLQGG[SA]YLP[G]

PTCH 251 KPPLRWTNFDPLEFLEELKKINYQVDSWE[EM]LNKAEVGHGYMDR[PC]LNPA  
PTCH2 208 RPDIQWTNLDPEQLLEELGPFA.SLEGFR[EL]LDKAQV[GQ]AYVGR[PC]LHPD

PTCH 301 DPDCPATAPNKNSTKPLDMA[LV]LNGGCHGLS[RKY]MHWQEELIVGGTVKNS  
PTCH2 257 DLHCP[PS]APNHHS[RO]APNV[A]HEL[SGGCH]GFS[HK]F[MHWQEEL]LLGGMARDP

PTCH 351 TGKLVSAHALQTMFQLMTPKQMVEHF[KG]YEVSHITNWNEDKAAI[LE]AW  
PTCH2 307 QGELLRAEALQSTFELLMSPRQLYEHFRG.DYQTHDIGWSEEQASTVLQAW

TM2

PTCH 400 QRTYVEVVHQSV[AN]STQKVL[SF]TTTLDDILK[SF]SDSVIRV[AS]GYLLM  
PTCH2 356 QRRFVQLAQEALPE[NA]SQIHA[EF]STTLDDILH[AF]SEVSAARV[VG]GYLLM

FIG. 3A



FIG. 3B

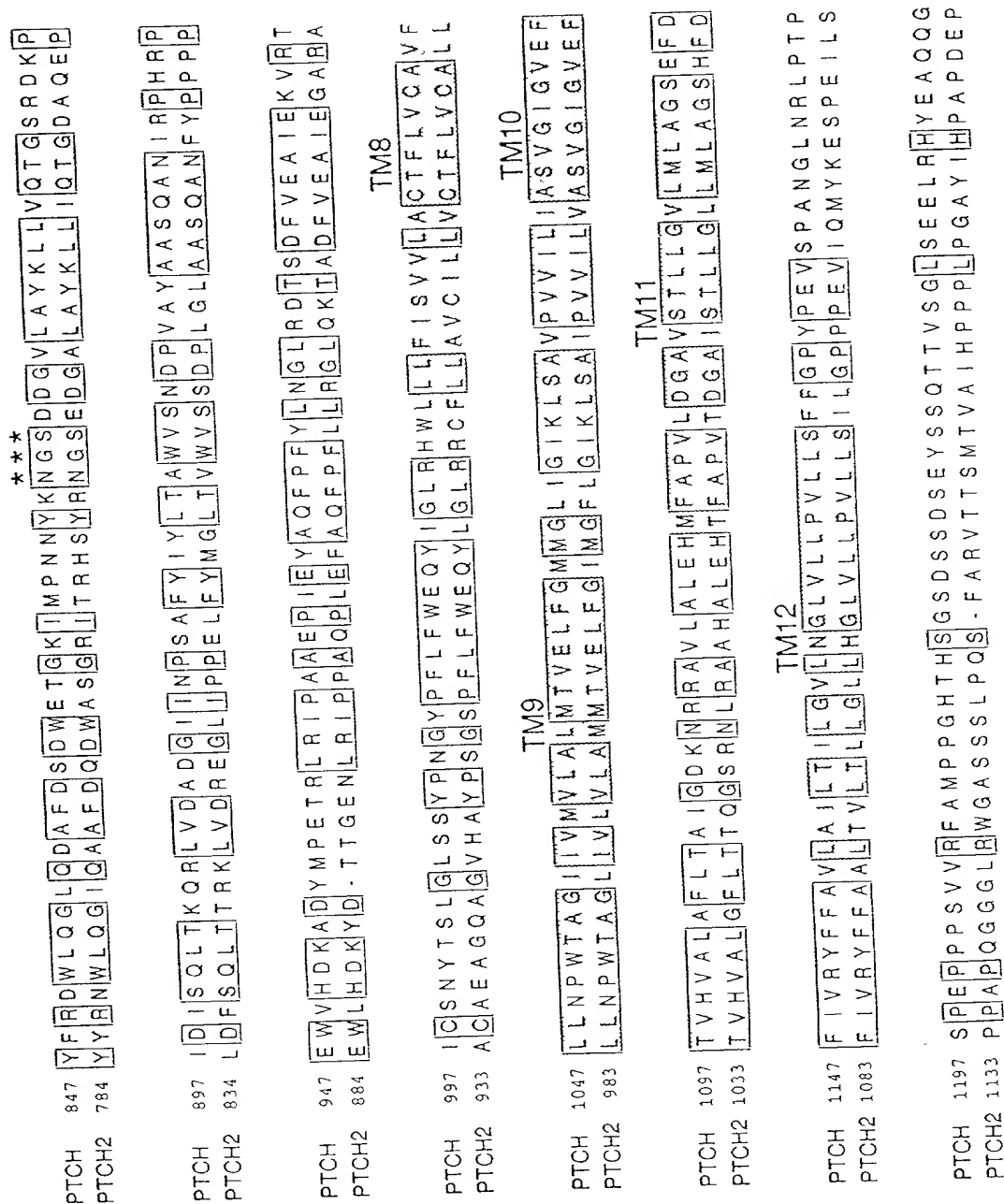
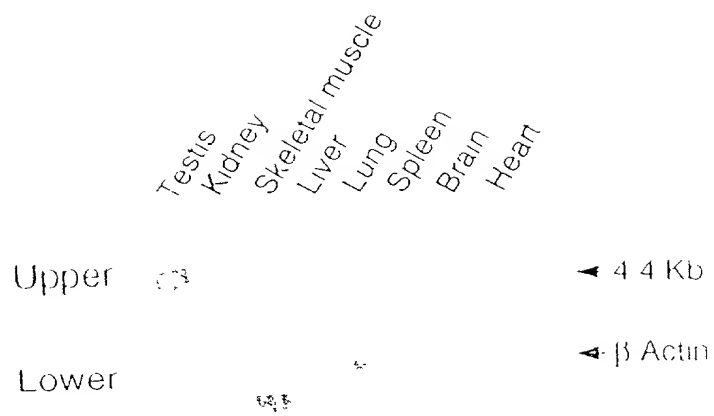


FIG. 3C

PTCH 1247 AGG PAHQVIVEATENPVFAHSTVVHPESRHHPPSNPRQQPHLDSGSLPPG  
 PTCH2 1182 PWS PAATSSGNLSSRGPGPATG  
 PTCH 1297 RQGQPPRRDPPREGLWPPLYRPRRDAFEISTEGHSGPSNRA R W G P R G A R S  
 PTCH 1347 HNPRNPASTAMGSSVPGYCQPIITVTASASVTVAVHPPVPVPGPGRNPRGG  
 PTCH 1397 LCPGYPETDHGLFEDPHVPFHVRCERRDSKVEVIELQDVECEEERPRGSSS  
 PTCH 1447 N

FIG. 3D



**FIG. 4**

09990042-11001

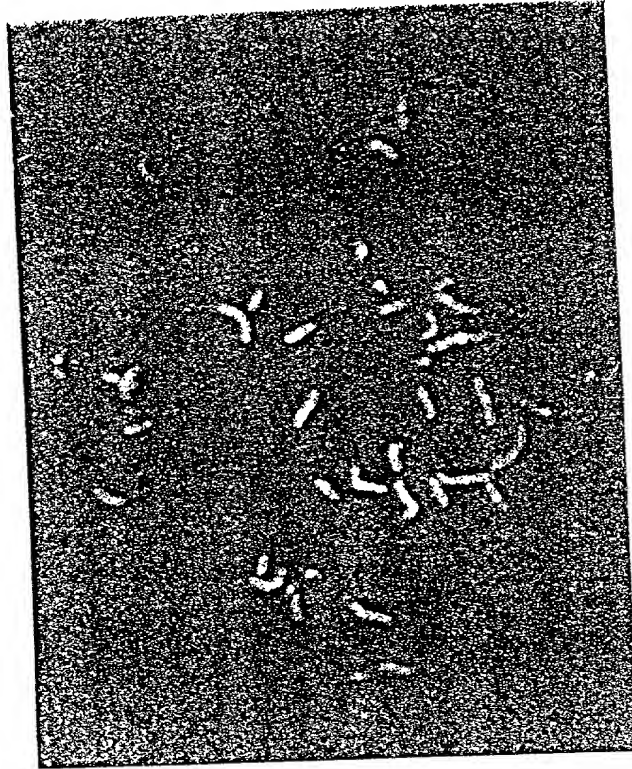


FIG. 5



FIG. 6A

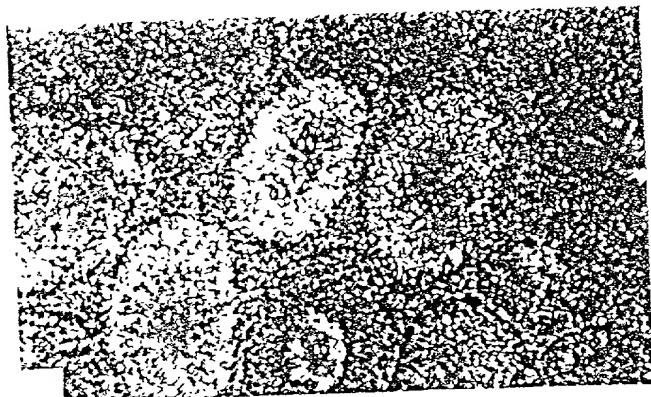


FIG. 6B

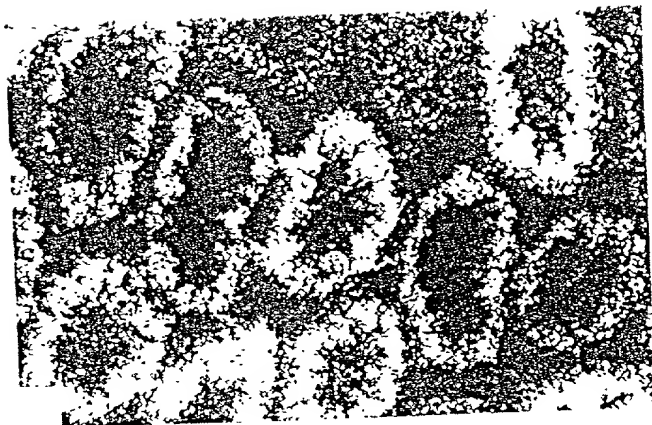


FIG. 6C

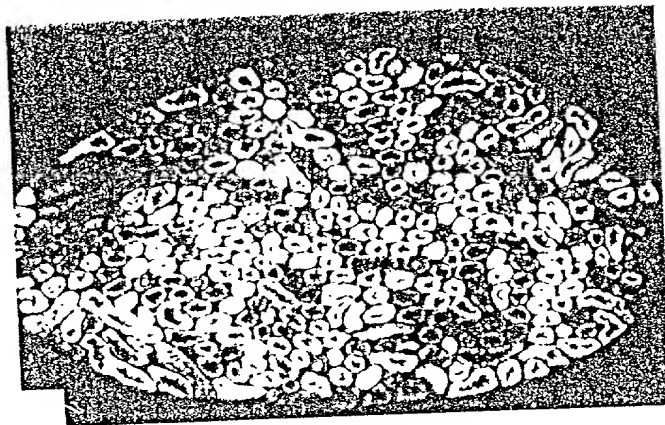


FIG. 6F

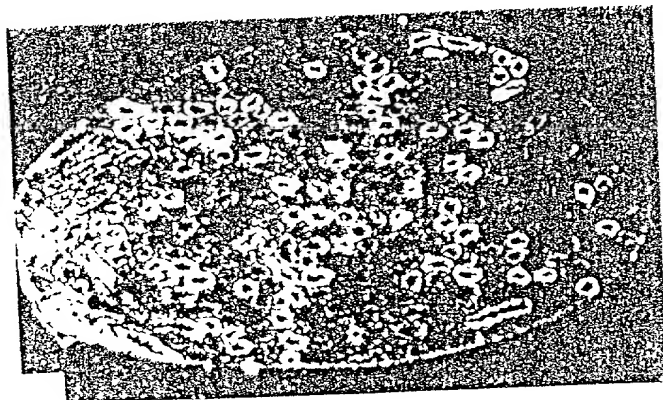


FIG. 6E

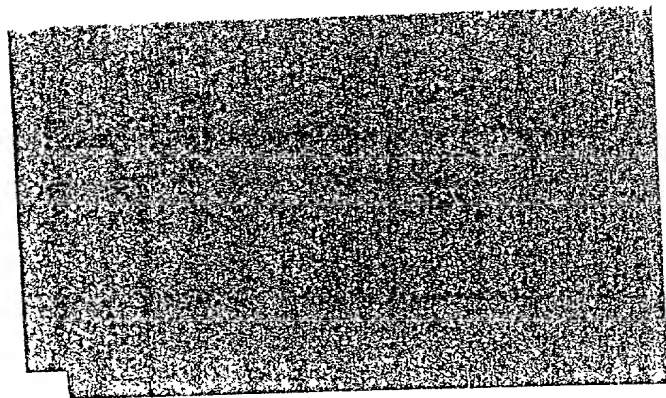


FIG. 6D

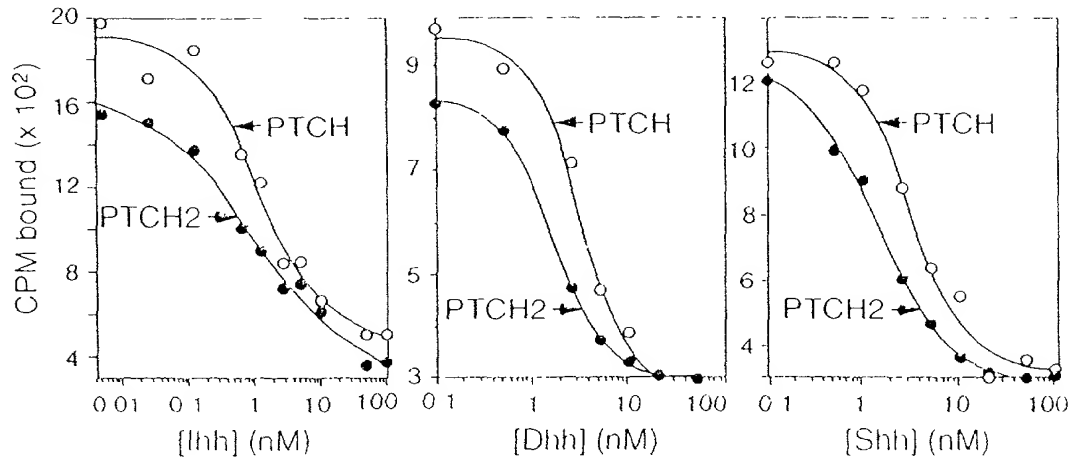


FIG. 7A

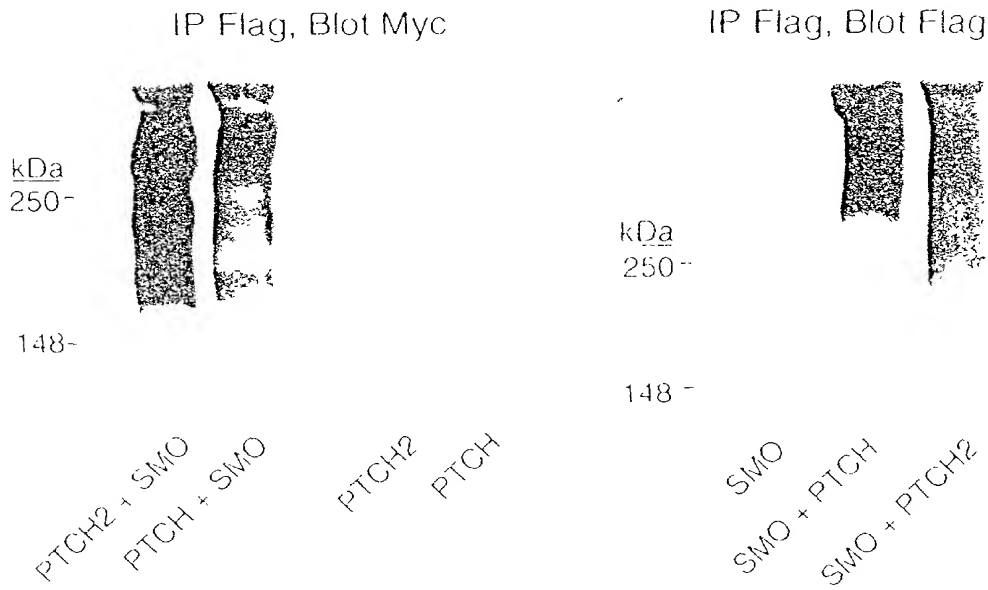


FIG. 7B



FIG. 8A

360 370 380 390 400  
*hPtc-2* VLQAWQRRFVQLAQEALPENASQQIHAFSSTLDDILHAFSEVSAARVVG  
 \*\*\*\*\*  
*mPatched2* VLQAWQRRFVQLAQEALPANASQQIHAFSSTLDDILRAFSEVSTTRVVG  
 360 370 380 390 400

410 420 430 440 450  
*hPtc-2* GYLLMLAYACVTMLRWDCAQSQSVGLAGVLLVALAVASGLGLCALLGIT  
 \*\*\*\*\*  
*mPatched2* GYLLMLAYACVTMLRWDCAQSQGAVGLAGVLLVALAVASGLGLCALLGIT  
 410 420 430 440 450

460 470 480 490 500  
*hPtc-2* FNAATTQVLPFLALGIGVDDVFLLAHAFTEALPGTPLQERMGECLQRTGT  
 \*\*\*\*\* \* \* \* \*  
*mPatched2* FNAATTQVLPFLALGIGVDDIFLLAHAFKAPPDTPPLPERMGECLRSTGT  
 460 470 480 490 500

510 520 530 540 550  
*hPtc-2* SVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFVAVMLVFPAIL  
 \*\* \* \* \* \*  
*mPatched2* SVALTSVNNMVAFFMAALVPIPALRAFSLQAAIVVGCNFAAVMLVFPAIL  
 510 520 530 540 550

560 570 580 590 600  
*hPtc-2* SLDLRRRHRCQRLDVLCCFSSPCSAQVIQILPQELGDGTVPVGIAHLTATV  
 \*\*\*\*\*  
*mPatched2* SLDLRRRHRCQRLDVLCCFSSPCSAQVIQMLPQELGDRAVPVGIAHLTATV  
 560 570 580 590 600

610 620 630 640 650  
*hPtc-2* QAFTHCEASSQHVVITILPPQAHLVPPSPDPLGSELFSPGGSTRDLLQEE  
 \*\*\*\*\*  
*mPatched2* QAFTHCEASSQHVVITILPPQAHLLSPASDPLGSELYSPGGSTRDLLSQEE  
 610 620 630 640 650

660 670 680 690 700  
*hPtc-2* ETRQKAACKSLPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLS  
 \* \* \* \* \*  
*mPatched2* GTGPQAACRPLLCAHWTLAHFARYQFAPLLLQTRAKALVLLFFGALLGLS  
 660 670 680 690 700

FIG. 8B

710 720 730 740 750  
 h*Ptch-2* LYGATLVQDGLALTDVVPRTKEHAFLSAQLRYFSLYEVALVTQGGFDYA  
 \*\*\*\*\*  
 mPatched2 LYGATLVQDGLALTDVVPRTKEHAFLSAQLRYFSLYEVALVTQGGFDYA  
 710 720 730 740 750

760 770 780 790 800  
 h*Ptch-2* HSQRALFDLHQRFSSLKAVLPPPATQAPRTWLHYYRNWLQGIQAAFDQDW  
 \*\*\*\*\*  
 mPatched2 HSQRALFDLHQRFSSLKAVLPPPATQAPRTWLHYYRSWLQGIQAAFDQDW  
 760 770 780 790 800

810 820 830 840 850  
 h*Ptch-2* ASGRITRHSYRNGSEDGALAYKLLIQTGDAQEPLDFSQLTTRKLV DREG  
 \*\*\*\*\*  
 mPatched2 ASGRITCHSYRNGSEDGALAYKLLIQTGNAQEPLDFSQLTTRKLV DKEGL  
 810 820 830 840 850

860 870 880 890 900  
 h*Ptch-2* IPPELFYMGLTVWVSSDPLGLAASQANFYPPPEWLHDKYDTTGENLRIP  
 \*\*\*\*\*  
 mPatched2 IPPELFYMGLTVWVSSDPLGLAASQANFYPPPEWLHDKYDTTGENLRIP  
 860 870 880 890 900

910 920 930 940 950  
 h*Ptch-2* PAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAEAGQAGVHAYPSGSP  
 \*\*\*\*\*  
 mPatched2 AAQPLEFAQFPFLLHGLQKTADFVEAIEGARAACAEAGQAGVHAYPSGSP  
 910 920 930 940 950

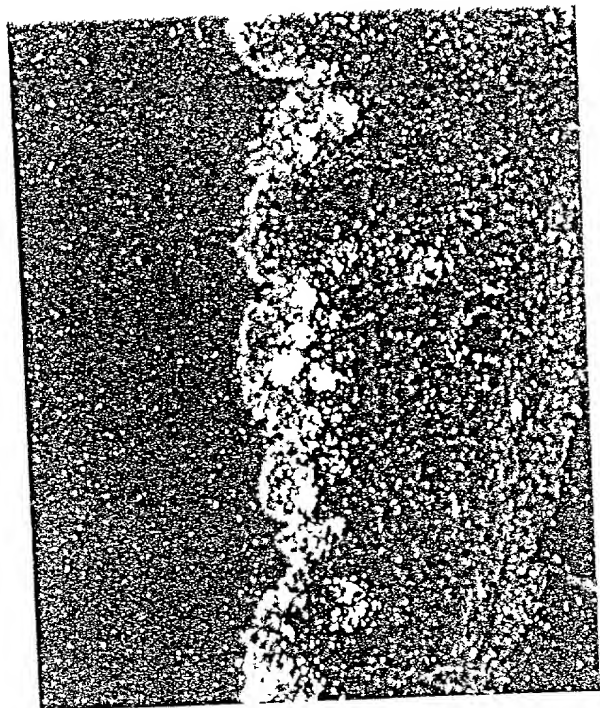
960 970 980 990 1000  
 h*Ptch-2* FLFWEQYLGLRRCFLLAVCILLVCTFLVCALLLLNPWTAGLIVLVLAMMT  
 \*\*\*\*\*  
 mPatched2 FLFWEQYLGLRRCFLLAVCILLVCTFLVCALLLLSPWTAGLIVLVLAMMT  
 960 970 980 990 1000

1010 1020 1030 1040 1050  
 h*Ptch-2* VELFGIMGFLGIKLSAIPVVILVASVGIGVEFTVHVALGFLT TQGSRLR  
 \*\*\*\*\*  
 mPatched2 VELFGIMGFLGIKLSAIPVVILVASIGIGVEFTVHVALGFLT SHGSRNLR  
 1010 1020 1030 1040 1050

FIG. 8C



PTCH2



PTCH

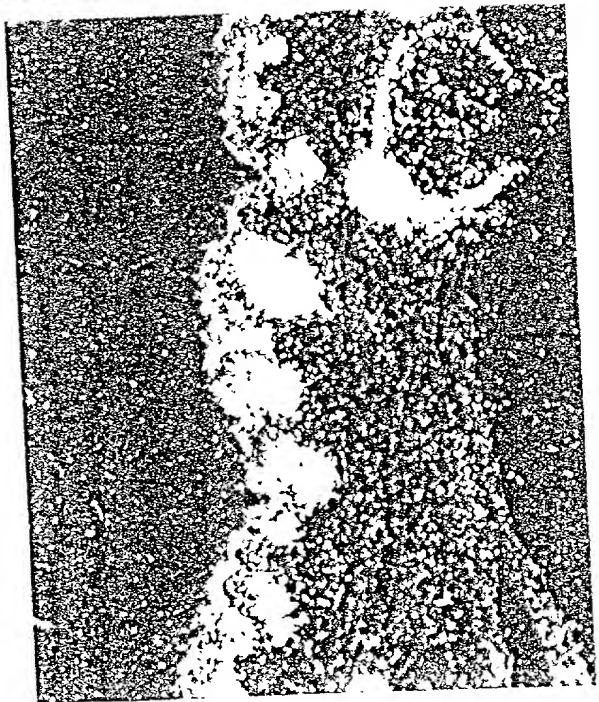


FIG. 9

> Consensus Sequence of human patched 2 cDNA clone  
> length: 4004 bp

(SEQ ID NO:8)

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1 CCCACGGGTC CGGAGAAAGC TGGGGGAGGA GGCTGCATAC ACCTCTCAGA TGCTGATACA GACCGCAGCG CAGGAGGGAG AGAATCTCTT CACACCCGAA
GGGTGCGCAG GGCCTCTTCG ACCCCCTCCT CCGACGATATG TGGAGATCTT race 6
101 GCACTTGGCC TCCACTCCCA GGCAGCCCTC ACTGCCAGTA AAGTCCAAAT ATCACTCTAT GGAAGTCTT GGAATTTGAA CAAAATCTGC TACAAGTCAG
CGTGAACCGG AGGTGGAGGT CCGTCGGGAG TGACGGTCTAT TTCAGGTTCA TAGTGAGATA CCCTTCAGGA CCTAAACTT GTTTTAGACG ATGTTCTAGTC race 5
201 GAGTTCCCTT TATTGAAAT GGAATGATTG AGCGGATGAT TGAGAAAGCTG TTTCCGTGCG TGATCCTCAC CCCCCTCGAC TGCTTCTGGG AGGAGGCCAA
CTCAAGGGGA ATAACTTTTA CCTTACTAAC TCGCCTACTA ACTCTTCGAC AAAGGCACGC ACTAGGAGTG GGGGAGCTG ACGAAGACCC TCCCTCGGTT
301 ACTCCAAGGG GGCTCCGCT ACCTGCCGCT CCCAATGTGG CTCACGAGCT GAGTGGGGG TGCCATGGCT TCTCCCACAA ATTATATGCAC TGGCAGGAGG
TGAGGTTCCC CCGAGGGCGA TGGACGGCGA GGGTTACACC GAGTGCTCGA CTCACCCCG ACGGTACCGA AGAGGGTGTT TAAGTACGTG ACCGTCTCTC
401 AATTGCTGCT GGGAGGCATG GCCAGAGACC CCCAAGGAGA GCTGCTGAGG GCAGAGGCC GTCAGAGCAC CTTCTTGCTG ATGAGTCCCC GCCAGCTGTA
TTAAGGACGA CCTCCGTAC CGGTCTCTGG GGGTTCTCTT CGACGACTCC CGTCTCCGG ACGTCTCTGT GAAGAACGAC TACTCAGGG CCGTCGACAT
501 CGAGCATTTT CCGGGTGACT ATCAGACACA TGACATTGGC TGGAGTGAGG AGCAGGCCAG CACAGTGCTA CAAGCTTGGC AGCGCGCTT TGTGCAGGTC
GTCGTAAAG GCCCACTGA TAGTCTGTGT ACTGTAACCG ACCTCACTCC TCGTCCGGTC GTGTCAAGAT GTTCGGACCG TCGCCCGGAA ACAGTCCAG
601 GGATATGGACA AGGACAGGGG GGTGCCCTGA GGCCATTCCC TCCTCCTGCC CCCTCCTATC CACCCTGTTT CTCACGCTGG CCCAGGAGGC CCTGCCTGAG
CCATACCTGT TCCTGTCCCC CCACGGGACT CCGGTAAGG AGGAGGACCG GGGAGGATAG GTGGGACAAA GAGGTGACCC GGTCTCTCCG GGACGGACTC
701 AACGCTTCCC AGCAGATCCA TGCCCTTCTCC TCCACCACCC TGGATGACAT CCTGCATGCG TTCTCTGAAG TCAGTGTGCTG CCGTGTGGTG GGAGGCTATC
TTGCGAAGGG TCGTCTAGGT ACGGAAGAG AGGTGGTGGG ACCTACTGTA GGACGTACGC AAGAGACTTC AGTCACGACG GGCACACCCAC CCTCCGATAG
801 TGCTCATGGT GGCTCTTGCA CCTGGCACCT TGCCCCCACC CCACCTCCAA CCAATGCCCA CCCTGGGGAG CCCCTGAGAC TGCCCTTTTC CCCCACAGCT
ACGAGTACCA CCCAGAACGT GGACCGTGA ACGGGGTGG GGTGGAGGTT GGTACAGGTT GGGACCCCTC GGGGACTCTG ACGGGAAGG GGGGTGTGGA

```

FIG. 10A

901 GGCCTATGCC TGTGTGACCA TGCTGCGGTG GGAAGTGGCC CAGTCCCAGG GTTCCCTGGG CCTGCGCGG GACTGCTGG TGGCCCTGSC GGTGGCCTCA  
CCGATACGG ACACACTGGT ACGACGCCAC CCTGACGCGG GTCAGGTCC CAAGGCACCC GGAAGGCCC CATGACGACC ACCGGGACCG CCACCGGAGT

1001 GGCCTTGGC TCTGTGCCCT GCTCGGCATC ACCTTCAATG CTGCCACTAC CCAGGTACGC CAGGACTGCA GGCAGACTC AGTGCCAGTC ACCAGGCTTC  
CCGAACCCG AGACACGGGA CGAGCCGTAG TGAAGTTAC GACGGTGATG GGTCCATGGG GTCTGACGT CCCGTCTGAG TCACGGTCAG TGGTCCGAAG

1101 ACGGGTCTC AGTGGCCGC TCCTCTGCC TCCTGCTCTT TGCCTTCTT GACTCTGGA ATCGCCTGG ATGACGTATT CCTGCTGGC CATGCCCTCA  
TGCCAGGAG TCGACGGCG AGGAGACGG GAGGTCCAC ACGGAAGAA CTGAGACCCT TAGCCGACC TACTGCATAA GGAAGACCG GTACGGGAAGT

1201 CAGAGGCTCT GCCTGGCACC CCTCTCCAGG TGGGSCCTTG TCCCCAGG CTCATCTGAG GCAGTACG TTAATGTTA AGAGCTCTT GTTCAAGTG  
GTCTCCGAGA CGGACCGTGG GGAGGGTCC ACCCGGAAC AGGGGTCCC GAGTAGACTC CGTCGAGTCG AATGACCAAT TCTCGGAGAA CCAAGTTTAC

1301 ACCTTGGGT GCTAATGAAC CTCGGTGCTT CTGTGCCCCA TGTGTAAACA GGGGAATAA TAGTGTGTG TCCTAAGGGT TATTGTTGG ATCAGTGAAG  
TGGAACCCGA CGATTACTG GAGCCACGGA GAACAGGGGT ACACATTGT CCCCCTTATT ATCAGACAC AGGATTCCCA ATAACAACC TAGTCACTTC

1401 TAATCAAGT TGAATGCTTA GAACAGCCCA TCATACGTAC ATGATACCA ATAAATGCTA GCCACTGTGT TATGACTGCC CCACCTCTGC ACCCAAGTT  
ATTGAGTTCA ACTTACGAAT CTGTGCGGT AGTATGCTATG TACCATGGGT TATTACGAT CGGTGACACA ATACTGACGG GTTGAGAGC TGGGTTCAA

1501 CCTGAGCTC CCTTCACTC CACTTTGACA CCGCCCCCTCC CTGTGACCT GAGGCGAGT CCCCCTCTG TCCTGGCAGG AGCGCATGG CGAGTGTCTG  
GGACTCGGAG GGAAGTGA GTGAACCTGT GCCGGGAGG GAACACTGGA CTCCTGTTCA CTTCCGTTCC GGGTGAGAC AGGACCGTCC TCGCGTACCC GCTCACAGAC

1601 CAGCGCACGG GCACAGTGT TGTACTACA TCCATCAACA ACATGGCCGC CTCTCTCATG GCTGCCCTCG TTCCCATCCC TGGCTGCGA GCCTTCTCCC  
GTCCGCTGCC CGTGGTACA ACATGAGTGT AGGTAGTTGT TGTACCGCG GAAGAGTAC CGACGGAGC AAGGTAGGG ACCTGACCT CGGAAGAGGG

1701 TACAGCCTGG ACCTACGGCG GCGCCACTGC CAGCGCCTTG ATGTGCTCG CTGCTTCTCC AGGTACTGCC TGGCCCCCAG CCCCCTCTC CCGTGACCCA  
ATGTCGGACC TGGATGCCG CGCGGTGACG GTCCCGAAC TACACGAGC GACGAAGAGG TCCATGACGG ACCTGGGTC GGGGAAGGAG GGCACCTGGT

1801 CGCCAGCCTG TCCCTCAC AGCATTTCAA GGCACAGACC TGTATCCAC TCTCTACCTC TTCAGTCCC TGCTCTGCTC AGGTGATTCA GATCCTGCCC  
GCGTCGGAC AGGGAGTGG TCGTAAAGTT CCGTGTCTGG ACAGTAGTG AGAGTGGAG AAGGTACGG ACAGACGAG TCCACTAAGT CTAGGACGGG

1901 CAGGAGCTGG GGGACGGGAC AGTACAGTG GGCATTGCCC ACCTCACTGC CACAGTTCAA GCCTTTACCC ACTGTGAGC CAGCAGCCAG CATGTGTCA  
GTCTCGACC CCTGCCCCG TCATGCTCAC CCGTAACGGG TGGAGTGAC GTGTCAAGT CCGAATGAGG TGACACTTCG GTGCTCGTC GTACACCAAGT

2001 CCATCCTGCC TCCCCAAGC CACCTGCTGC CCCCACCTC TGACCCACTG GGTCTGAGC TCTTACGCC TGGAGGTCC ACACGGGACC TTCTAGGCCA  
GTAGGACGG AGGGTTCCG GTGACCCACG GGGTGGAG ACTGGTGAC CCGAGACTCG AGAAGTCCG ACCTCCAGG TGTGCCCTGG AAGATCCGGT

FIG. 10B

2101 GGAGGAGGAG ACAAGGCAGA AGGACGCCTG CAAGTCCCTG CCTGTGCCC GCTGGAATCT TGCCATTTC GCCGCTATC AGTTTGCCCC GTTGCTGCTC  
CCTCCTCCTC TGTTCGGTCT TCCGTCCGAC GTTCAGGGAC GGGACACGGG CGACCTTAGA ACGGTAAAG CCGGCGATAG TCAACGGGG CAACGACGAG

2201 CAGTCACATG CCAAGGCCAT CGTGTGGTG CTCTTTGGTG CCTGAGCTC TACGAGCCA CCTTGGTGCA AGACGGCCTG GGCCTGACGG  
GTCAGTGATC GGTTCGGSTA GCACGACCAC GAGAACCAC GAGAAGACC GACTCGGAG ATGCTCGGT GGAACACCGT TCTGCCGGAC CGGGACTGCC

2301 ATGTGGTGCC TCGGGGCACC AAGGAGCATG CCTTCTGTAG CGCCAGCTC AGGTACTTCT CCCTGTACGA GTGGCCCTG GTGACCCAGG GTGGCTTTGA  
TACACCACGG AGCCCGTGG TTCTCTGTAC GGAAGGACTC GCGGTCGAG TCCATGAAGA GGGACATGCT CCACCGGAC CACTGGGTCC CACCGAAACT

2401 CTACGCCAC TCCCAACGG CCTCTTTGA TCTGCACCAG CGCTTCAGTT CCTCAAGGC GTGTGTCCTC CCACCGGCCA CCGAGGCACC CCGCACCTGG  
GATCGGGTG AGGTTGGC GGGAGAACT AGACGTGGTC GCGAAGTCAA GGGAGTTCCG CCACGACGGG GTGGCCGGT GGGTCCGTG GCGTGGAC

2501 CTGCACTATT ACCGCAACTG GCTACAGGGA ATCCAGGCTG CCTTTGACCA GGAAGTGGT TCTGGGGCCA TCACCCGCCA CTCGTACCGC AATGGCTCTG  
GACGTGATAA TGGGTTGAC CGATGTCCT TAGGTCCGAC GGAAGTGGT CCTGACCCGA AGACCCCGT AGTGGCGGT GAGCATGGC TTACCGAGAC

2601 AGGATGGGC CTGGCCCTAC AAGCTGCTCA TCCAGACTGG AGACGCCCG AGCCCTCTGG ATTTACGCCA GGTGGGAGA GGGCTGGAGG GTTCCACTAG  
TCCTACCCCG GGACCGGATG TTCGACGAGT AGGTCTGACC TCTGCGGTC CTGCGAGACC TAAAGTCGT CCAACCTCT CCGACCTCC CAGGTGATC

2701 TACAGGGCT GCAGCCCTCC TGGGCCCCAG CCTTCAGCCC TCTCTGCTC TGCACTGAC CACAAGGAAG CTGGTGGACA GAGAGGACT GATTCCACCC  
ATGTCCCGGA CGTCCGGAG ACCCGGGTCC GGAAGTCGGG AGAGACGGAG ACGTCACTG GTGTCTCTC GACCACCTGT CTCTCCCTGA CTAAGGTGGG

2801 GAGCTCTTCT ACATGGGGCT GACCGTGTGG GTGAGCAGTG ACCCCCTGGG TCTGGCAGCC TCACAGGCCA ACTTCTACCC CCCACCTCT GAATGGCTGC  
CTCGAGAAGA TGTACCCCGA CTGGCACACC CACTCGTCA CACTCGTCA TGGGGGACCC AGACCGTCGG AGTGTCCGT TGAAGATGG GGGTGGAGA CTTACCGACG

2901 ACGACAAATA CGACACCACG GGGGAGAACC TTCGCAGTGA GTCTTGGGG GAGCTCGCA AGAGCCTCAG CCTCGCCCA CAAAGCCCTG AGCCTGAGGC  
TGCTGTTTAT GCTGTGGTGC CCCCCTTGG AAGCGTCACT CAGAACCCCT CTGAGCCGT TCTCGGAGTC GGAGCGGGT TGTTCGGAC TCGACTCCG

3001 CTGCCCCACT CTGCCCCGTG CTCACCGCCC TGTCCCTCTC CTCTTCTCC CCTCCACAGT CCGGCCAGCT CAGCCCTGG AGTTTCCCCA  
GGACGGGTGA GACGGGCAC GAGTGGCGG ACAGGGAGAG GGAGAAGAG GAAGGGAGG GGAGGTGTCA GGGCGGTCCA GTCCGGAAC TCAAACGGGT

FIG. 10C



3101 GTTCCCTTC CTGCTGGTG GCCTCAGAA GACTGCAGAC TTTGTGGAG CCATCGAGG GCGCCGGGCA GCATGCGCAG AGCCCGGCA GGCTGGGTG  
CAAGGGAAG GACGACGCAC CGGAGGTCTT CTGACGTCTG AAACACCTCC GGTAGCTCCC CCGGGCCCGT CGTAGCGGTC TCCGGCCGGT CCGACCCAC

3201 CACGCTACC CCAGCGGCTC CCCCTTCCTC TTCTGGGAAC AGTATCTGG CCTGCGGGGC TGCCTCTGC TGGCGTCTG CATCCTGCTG GTGTGCACTT  
GTGCGATGG GGTGCGCGAG GGGGAAGGAG AAGACCTTG TCATAGACC GGACGCCCG ACGAAGGACG ACCGCGAGAC GTAGGACGAC CACACGTGAA

3301 TCCTCGTCTG TGGCTGTGTC CTCCTCAACC CCTGGACGGC TGGCTCATA GTGAGTGCTT GCAGGAGTGG GGACAGAGAC ACCCACCTT TCCCTGCCCA  
AGGAGCAGAC ACAGACGAC GAGGAGTTGG GACCTGCCG GAGCAGTAT CACTCACGAA CGTCTCACC CCTGTCTG TGGGTGGG AGGACGGGT

3401 GCCTGTCATC CCTCTGCCA GGAGCCCTCT GTAGCCCTG TCTCCCTCAG GTGCTGTCC TGGCGATGAT GACAGTGA GATCTTTGTA TCATGGGTTT  
CGGACAGTAG GGAGACGGT CCTCGGGAGA CACTCGGGAC AGAGGAGTC CAGGACCAG CAGGCTACTA CTGTACCTT GAGAAACCAT AGTACCCAAA

3501 CCTGGGCATC AAGCTGAGTG CCATCCCCGT CCATCCCCGT GTGATCCTT GTGGCCTCTG TAGGCATTGG CGTTGAGTTC ACAGTCCACG TGGCTCTGGT GAGCACGGG  
GGACCCGTAG TTCGACTCAC GGTAGGGGCA CCACTAGGAA CACCGGAGAC ATCCGTAACC GCAACTCAAG TGTCAGGTGC ACCGAGACCA CTCGTGCCCC

3601 ACCCCGGGGA GGGACCAATC AGCTGATTCA GTATTCAACA CATATTCTC AAGCCCTAC TATGTGCTAG GTACTATTTA AGAATTTGG CTGGGTGGAC  
TGGGGCCCCC CCTGGTTAG TCGACTAAGT CATAAGTTGT GTATAACAAG TTCGGGATG ATACACGATC CATGATAAAT TCTTAAACCC GACCCACCTG

3701 GTGGTGGTTC ATTCCTGTAA TCCAGCACT TTGGGAGGCC GAGCGGGTG GATCACCTGA GGTGCGGAGT TCGAAACGAG CCTGGCCAAC ATGGTGAAC  
CACCACCGAG TAAGGACATT AGGTCTGTGA AACCTCCCG CTCCGCCAC CTAGTGGACT CCAGCCCTCA AGCTTTGGTC GGACCGGTTG TACCACCTTG

3801 CCTGTCTTTA CTAAAATAC AAAAAATTAG CCAGGCGTGG TGGCACATGC CAGTAGTCCC AGCTACTTTG GAGGCTGAGG CAGAATTGCT TGAACTGGG  
GGACAGAAAT GATTTTATG TTTTAAATC GGTCCGCACC ACCGTGTACG GTCATCAGGG TCGATGAAAC CTCCGACTCC GTCTTAACGA ACTTGGACCC

3901 AGGCGAAGGT TGCAGTGAGC TGAGATCGTG CCATTGCACT CCAGCCTGG CAACAAGAGT GCAACTCTCC GTCTCAAAA AAAAAAAA AAGGCGGGC  
TCCGCTTCCA ACGTCACTCG ACTCTAGCAC GGTAACTGA GGTGCGACCC GTTGTCTCA GGTGAGAGG CAGAGTTTTT TTTTTTTTTT TTCCCGCCGG

4001 GCGA  
CGCT

FIG. 10D

Clone 16.1 human patched 2

> length: 2082 bp

> (SEQ ID NO:9)

```

1  TTCCGGCATG ACTGATCGC CCCCCCTCAG AGAGCTGCCC CCGAGTTACA CACCCCAGC TCGAACCGCA GCACCCCCAGA TCCTAGCTGG GAGCCTGAAG
   AAGGCGGTAC TGAGCTAGCG GCGGGGAGTC TCTCGACGGG GGCTCAATGT GTGGGGTGG AGCTTGGCGT CGTGGGGTCT AGGATCGACC CTCGGACTTC
101 GCTCCACTCT GGCTTCGTGC TTACTTCCAG GGCCTGCTCT TCTCTCTGGG ATGCGGATC CAGAGACATT TTGGCAAAGT GCTCTTTCTG GGAAGTGGG
   CGAGGTGAGA CCGAAGCAGC AATGAAGTC CCGGACGAGA AGAGAGACCC TACGCCCTAG GTCTCTGTAA CACCGTTTCA CGAGAAAGAC CCTGACAAAC
201 CCTTTGGGC CCTGGCATTA GGTCTCCGCA TGGCCATTAT TGAGACAAAC TTGGAACAGC TCTGGGTAGA AGTGGGCAGC CGGGTGAGCC AGGAGCTGCA
   GGAACCCCG GGACCGTAAT CCGAGAGCGT ACCGGTAATA ACTCTGTTG AACCTTGTG AGACCATCT TCACCCGTCG GCCACTCGG TCCTCGACGT
301 TTACACCAAG GAGAAGCTGG GGGAGGAGGC TGCATACACC TCTCAGATGC TGATACAGC CGCACGCCAG CGGAGAGAGA ACATCCTCAC ACCCGAAGCA
   AATGTGTTTC CTCTTCGACC CCTCCTCCG ACGTATGTGG AGAGTCTACG ACTATGTCTG CGGTGCGGTC CTCCCTCTCT TGTAGGAGTG TGGGCTTCGT
401 CTTGGCCTCC ACCTCCAGGC AGCCCTCACT GCCAGTAAAG TCCAAGTATC ACTCTATGGG AAGTCCCTGGG ATTGAAACAA AATCTGCTAC AAGTCAGGAG
   GAACCGGAGG TGGAGTCCG TCGGGAGTGA CCGTCAATTC AGGTCATAG TGAGATACCC TTCAGGACCC TAAACTTGT TTAGACGATG TTCAGTCTCT
501 TTCCCTTTAT TGAAAATGGA ATGATTGAGT GGATGATTGA GAAGCTGTTT CCGTGGTGA TCCTCACCCC CCTCGACTGC TTCTGGGAGG GAGCCAAACT
   AAGGGGAATA ACTTTTACCT TACTRACTCA CCTACTAACT CTTGACAAA GGCACGCACT AGGAGTGGG GGAGCTGACG AAGACCTCC CTCGGTTTGA
601 CCAAGGGGGC TCCGCCCTACC TGCCCGGGCGG CCGGGATATC CAGTGGACCA ACCTGGATCC AGAGCAGCTG CTGGAGGAGC TGGTCCCTT TGCCTCCCTT
   GGTTCCTCCG AGGCGGATGG ACGGGCGGCG CCGGCTATAG GTCACCTGGT TGBACCTAGG TCTCGTCGAC GACCTCCTCG ACCAGGGAA ACGGAGGGAA
701 GAGGGCTTCC GGGAGCTGCT AGACAAGGCA CAGGTGGGCC AGGCCTACGT GGGGCGGCC TGCTTGCACC CTGATGACCT CCACTGCCCCA CCTAGTCCCC
   CTCCGAAGG CCTCGACGA TCTGTTCCGT GTCCACCCGG TCCGGATGCA CCCCAGCGG ACAGACGTGG GACTACTGGA GTGACGGGT GGTACAGGG
801 CCAACCATCA CAGCAGGCAG GCTCCCAATG TGGCTACGA GCTGAGTGGG GGCTGCCATG GCTTCTCCCA CAAATTCATG CACTGGCAGG AGGAATTGCT
   GGTGGTAGT GTGCTCCGTC CGAGGGTTAC ACCAGTGTCT CGACTCACC CCGACGGTAC CGAAGAGGGT GTTTAAGTAC GTGACCGTCC TCCTTAACGA
901 GCTGGGAGGC ATGGCCAGAG ACCCCCAAGG AGAGCTGCTG AGGGCAGAGG CCCTGACAG CACCTTCTTG CTGATGAGTC CCCGCCAGCT GTACGAGCAT
   CGACCTCCG TACCGGTCTC TGGGGTTCC TCTCGACGAC TCCCCTCTCC GGGAGCTCTC GTGGAAGAAC GACTACTCAG GGGCGGTGCA CATGCTCGTA

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FIG. 11A

1001 TTCCGGGGTG ACTATCAGAC ACATGACATT GGCTGAGTG AGGACAGGC CAGACAGTG CTACAAGCCT GGCAGCGGCG CTTTGTGCAG CTGGCCCCAGG  
AAGGCCCCAC TGATAGTCTG TGTACTGTAA CCGACCTCAC TCCTCGTCCG GTCGTGTCAC GATGTTCCGA CCGTCGCCGC GAAACAGTC GACCCGGTCC

1101 AGGCCCTGCG TGAGAACGCT TCCCAGCAGA TCCATGCTTT CTCCTCCACC ACCTGGATA ACATCCTGCA TCGGTTCTCT GAAGTCAGTG CTGCCCGTGT  
TCCGGACGG ACTCTTGCA AGGTCTGCT AGGTACGAA GAGGAGGTGG TGGACCTAT TGTAGGACGT ACGCAAGAGA CTTACGTCAC GACGGGCACA

1201 GGTGGGAGGC TATCTGCTCA TGCTGGCTTA TGCCTGTGTG ACCATGCTGC GGTGGGACTG CGCCCCAGTC CAGGGTTCCG TGGGCTTGC CGGGGTACTG  
CCACCTCCG ATAGACGAGT ACGACCGGAT ACGGACACAC TGGTACGAG CCACCTGAC GCGGGTCAGG GTCCCAAGGC ACCCGAAGC GCCCCATGAC

1301 CTGTGGGCC TGGCGGTGGC CTCAGGCCCTT GGGCTCTGTG CCCTGCTCGG CATCACCTTC AATGCTGCCA CTACCAGGT GTGCCCTTC TTGGCTCTGG  
GACCACCGG ACCGCCACG GAGTCCGAA CCGAGACAC GGGACGAGC GTAGTGAAG TTACGACGCT GATGGTCCA CGACGGGAAG AACCGAGAC

1401 GAATCGGCGT GGATGACGTA TTCCTGCTGG CGCATGCTCT CACAGAGGCT CTGCTGCGCA CCCCTCTCCA GGAGCGCATG GCGAGTGTG TGCAGCGCAC  
CTTAGCCGA CCTACTGCAT AAGGACGACC GCGTACGAA GTGTCTCCGA GACGACCGT GGGGAGAGT CCTCGCGTAC CCGTCAACAG ACGTCGCGTG

1501 GGGACACAGT GTCGTACTCA CATCCATCAA CAACATGGCC GCCTTCTCTA TGGCTGCCCT CGTTCCCATC CCTGCGTGC GAGCCTTCTC CTTACAGCCA  
CCCGTGTCA CAGCATGAGT GTAGGTAGT GTGTACCG GGAAGAGT ACCGACGGA GCAAGGTAG GGACGCGAG CTCGGAGAG GAATGTCGT

1601 TCCTCAGCCT GGACCTACGG CGGCGCCACT GCCAGGCTT TGATGTGCTC TGCTGCTCT CCAAGTCCCTG CTCTGCTCAG GTGATTGAGA TCCTGCCCCA  
AGGAGTCGA CCGGATGCC GCGCGGTGA CCGTCCGGA ACTACACGAG ACGACGAGA GTCAAGTTCG GAAATGGTG AACTTCCGT GTCGGTCTG ACACCACTGG

1701 GGAGCTGGG GACGGGACAG TACCAGTGG CATTGCCAC CTCACTGCCA CAGTTCAAGC CTTTACCCAC TGTGAAGCCA GCAGCCAGCA TGTGTCACC  
CCTCGACCC CTGCCCTGTC ATGGTCACCC GTAACGGGTG GTAGTACGCT GAGTACGCTG TGGTGACCC GAGACTCGAG AAGTCGGGAC CTCCCAGTG TGCCCTGGAA GATCCGGTCC

1801 ATCCTGCCTC CCCAAGCCCA CCTGGTGCCC CCACCTTCTG ACCCACTGGG CTCTGAGCTC TTCAGCCCTG GAGGGTCCAC ACGGACCTT CTAGGCCAGG  
TAGGACGGAG GGGTTCGGT GGACCAACGG GTTGAAGAC TGGTGACCC GAGACTCGAG AAGTCGGGAC CTCCCAGTG TGCCCTGGAA GATCCGGTCC

1901 AGGAGGAGAC AAGGCAGAAG GCAGCCTGCA AGTCCCTGCC CTGTGCCCGC TGGAACTTG CCCATTTCGC CCGGAATTC CTGCAGCCCG GGGGATCCAC  
TCCTCCTCTG TTCCGTCCTC CGTCGGACGT TCAGGGACCG GACACGGCG ACCTTAGAAC GGGTAAAGCG GGGCTTAAG GACGTCGGG CCCCCTAGTG

2001 TAGTCTCTAGA GCGGCCGCCA CCGCGGTGSA GCTCAGCTT TTGTTCCCTT TAGTGAGGT TAATTGCGG CTTGGGTATC TT  
ATCAAGATCT CGCCGGCGGT GCGGCCACCT CGAGGTGAA AACAGGGAA ATCACTCCA ATTAACGCGC GAACCCATAG AA

FIG. 11B